

# FLY GENETICS LAB

## Experiment 1 – Single Trait: Simple Recessive Inheritance

Apterous wing size is recessive to wild-type wing size. Show the cross for a wild type female with an apterous wing male. Calculate the **expected frequency** from the cross. Perform the cross with these flies in the simulation. Use the **observed numbers** from the simulation to calculate the **expected number**. Use the simulation to conduct a chi square.



Total Offspring: \_\_\_\_\_

Trait	Expected Frequency	Observed Number	Expected Number
Wild Type			
Apterous			

Null Hypothesis: The observed number of flies with each trait variation will be no different from the expected number of flies with each trait variation.

Reject or Accept Decision:

Use one of the F1 flies as each new parent. Fill in data table & conduct Chi square test as in the previous example.



Total Offspring: \_\_\_\_\_

<b>Trait</b>	<b>Expected Frequency</b>	<b>Observed Number</b>	<b>Expected Number</b>
Wild Type			
Apterous			

Null Hypothesis: The observed number of flies with each trait variation will be no different from the expected number of flies with each trait variation.

Reject or Accept Decision:

## **Experiment 2 - Single Trait: X-Linked Recessive Inheritance**

**Yellow body color is recessive** to **wild-type body color** and is also located on the **X-chromosome**. Show the cross for a wild type female with a yellow male. Fill in data table & conduct Chi square test as in the previous examples.


Total Offspring: \_\_\_\_\_

Trait	Expected Frequency	Observed Number	Expected Number
Wild Type Females			
Wild Type Males			
Yellow Females			
Yellow Males			

Null Hypothesis: The observed number of flies with each trait variation will be no different from the expected number of flies with each trait variation.

Reject or Accept Decision:

Show the cross for an F1 female with an F1 male. Fill in data table & conduct Chi square test as in the previous examples.



Total Offspring: \_\_\_\_\_

Trait	Expected Frequency	Observed Number	Expected Number
Wild Type Females			
Wild Type Males			
Yellow Females			
Yellow Males			

Null Hypothesis: The observed number of flies with each trait variation will be no different from the expected number of flies with each trait variation.

Reject or Accept Decision:

### Experiment 3 - Single Trait: X-Linked Dominant Inheritance

**Bar Eye shape is dominant** to **wild-type eye shape** and is also located on the **X-chromosome**. Show the cross for a Bar eye female with a wild type male. Calculate the **expected frequency** from the cross... **NOTE: You are not told whether the Bar-eye female is *heterozygous* or *homozygous dominant*. Take a guess!** Fill in data table & conduct Chi square test as in the previous examples.



Total Offspring: \_\_\_\_\_

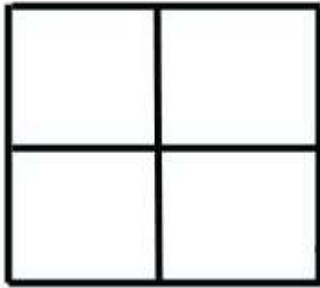
Trait	Expected Frequency	Observed Number	Expected Number
Wild Type Females			
Wild Type Males			
Bar Eye Females			
Bar Eye Males			

Null Hypothesis: The observed number of flies with each trait variation will be no different from the expected number of flies with each trait variation.

Reject or Accept Decision:

**If your initial guess was wrong, change the data above to reflect the CORRECT genotype of the female...OR do the computer cross before filling in the data table & Punnett square.**

Show the cross for heterozygous Bar eye female with a wild type male. Fill in data table & conduct Chi square test as in the previous examples.



Total Offspring: \_\_\_\_\_

Trait	Expected Frequency	Observed Number	Expected Number
Wild Type Females			
Wild Type Males			
Bar Eye Females			
Bar Eye Males			

Null Hypothesis: The observed number of flies with each trait variation will be no different from the expected number of flies with each trait variation.

Reject or Accept Decision:

#### **Experiment 4 – Two Trait Cross I**

Brown eyes & Spineless bristles are recessive to wild type eye color & wild type bristles. Show the cross for a Wild Type female with a brown eye, spineless bristle male. Fill in data table & conduct Chi square test as in the previous examples.


Total Offspring: \_\_\_\_\_

<b>Trait</b>	<b>Expected Frequency</b>	<b>Observed Number</b>	<b>Expected Number</b>
Wild Type Eye Color/Wild Type Bristles			
Wild Type Eye Color/Spineless Bristles			
Brown Eyes/Wild Type Bristles			
Brown Eyes/Spineless Bristles			

Null Hypothesis: The observed number of flies with each trait variation will be no different from the expected number of flies with each trait variation.

Reject or Accept Decision:

Attempt to determine if the gene for eye color & bristles are on separate chromosomes (un-linked genes) or on the same chromosome (linked genes) by crossing a dihybrid female (heterozygous for both traits) with a dihybrid male. Calculate the **expected frequency** from the cross, **assuming they are unlinked genes**. Fill in data table & conduct Chi square test as in the previous examples.


Total Offspring: \_\_\_\_\_

Trait	Expected Frequency	Observed Number	Expected Number
Wild Type Eye Color/Wild Type Bristles			
Wild Type Eye Color/Spineless Bristles			
Brown Eyes/Wild Type Bristles			
Brown Eyes/Spineless Bristles			

Null Hypothesis: The observed number of flies with each trait variation will be no different from the expected number of flies with each trait variation.

Reject or Accept Decision; also include a rationale for how you know they are linked or unlinked genes:



### **Experiment 5 – Two Trait Cross II**

Curved wings & Black body color are recessive to wild type wings & wild type body color. Show the cross for a Wild Type female with a curved wing, black body color male. Fill in data table & conduct Chi square test as in the previous examples.


Total Offspring: \_\_\_\_\_

<b>Trait</b>	<b>Expected Frequency</b>	<b>Observed Number</b>	<b>Expected Number</b>
Wild Type Body Color/Wild Type Wings			
Wild Type Body Color/Curved Wings			
Black Body/Wild Type Wings			
Black Body/Curved Wings			

Null Hypothesis: The observed number of flies with each trait variation will be no different from the expected number of flies with each trait variation.

Reject or Accept Decision:

Attempt to determine if the gene for body color & wings are on separate chromosomes (un-linked genes) or on the same chromosome (linked genes) by crossing a dihybrid female (heterozygous for both traits) with a black body color, curved wing male. Calculate the **expected frequency** from the cross, **assuming they are unlinked genes**. Fill in data table & conduct Chi square test as in the previous examples.


Total Offspring: \_\_\_\_\_

Trait	Expected Frequency	Observed Number	Expected Number
Wild Type Body Color/Wild Type Wings			
Wild Type Body Color/Curved Wings			
Black Body/Wild Type Wings			
Black Body/Curved Wings			

Null Hypothesis: The observed number of flies with each trait variation will be no different from the expected number of flies with each trait variation.

Reject or Accept Decision; also include a rationale for how you know they are linked or unlinked genes:

## **Experiment 6** – Gene Map for Linked Genes

The genes for **Dumpy wing shape**, **Purple eye color** and **Black body color** are all located on an autosome and are recessive traits. Perform crosses that will determine a relative gene map showing the distances and positions of these 3 genes on the chromosome. Note- these data may not add up exactly to a precise gene map.

Basic steps

1. Cross wild type female with male recessive for both traits.
2. Mate an F1 female with a parental male from 1<sup>st</sup> cross.
3. Send data to computer; calculate recombination frequency to obtain distance between the 2 genes. (multiply the frequency by 100 for a whole number).
4. Repeat for other trait crosses & fill in table below.

<b>Traits</b>	<b>Distance between the 2 genes</b>
Dumpy Wings & Purple Eyes	
Dumpy Wings & Black Body	
Purple Eyes & Black Body	

Plot where the genes would be approximately located on the chromosome model below.



### **Optional Extension Assessment**

Anyone who finishes early or wishes to do an inquiry based activity can complete the assessment below for an optional **20 Point Exam Grade**

For any traits **NOT** used in any preceding problems:

1. **Identify** an autosomal recessive trait, show the **parental cross** and **F1 cross** as Punnett squares, and write an explanation of how the simulation fly numbers/frequencies support its classification as an autosomal recessive trait.
2. **Identify** an X-linked recessive trait, show the **parental cross** and **F1 cross** as Punnett squares, and write an explanation of how the simulation fly numbers/frequencies support its classification as an X-linked recessive trait.
3. **Identify** an autosomal dominant trait, show the **parental cross** and **F1 cross** as Punnett squares, and write an explanation of how the simulation fly numbers/frequencies support its classification as an autosomal dominant trait.
4. **Identify** an autosomal dominant LETHAL trait, show the **parental cross** and **F1 cross** as Punnett squares, and write an explanation of how the simulation fly numbers/frequencies support its classification as an autosomal dominant LETHAL trait.
  - **Note – LETHAL dominant traits always means that a homozygous dominant DIE and therefore are not possible as a genotype...therefore all dominant phenotypes must be heterozygous.**
5. **Identify** 2 linked genes, show the **parental cross** and **F1 cross** as Punnett squares, and write an explanation of how the simulation fly numbers/frequencies support their classification as linked genes.